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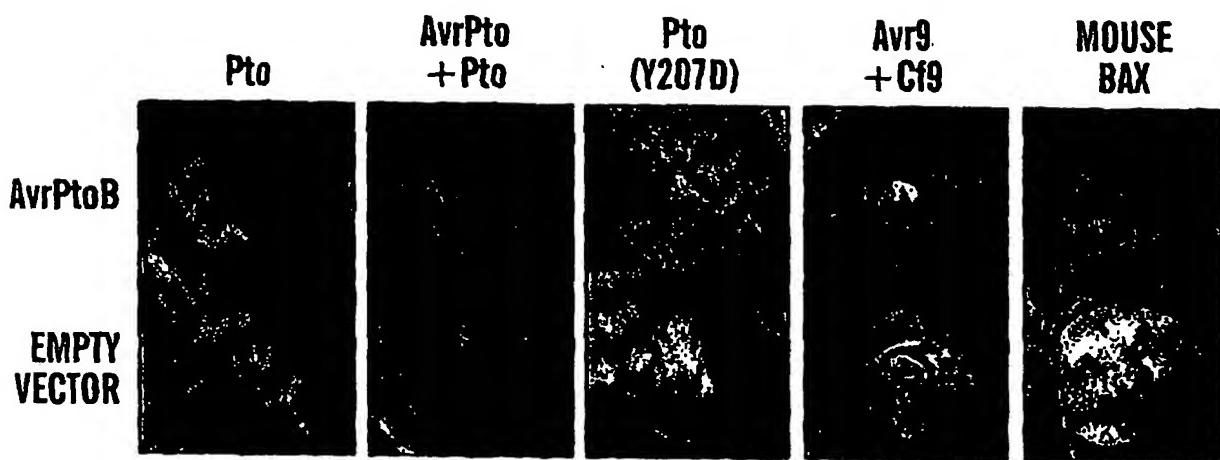


FIG. 1A



FIG. 1B

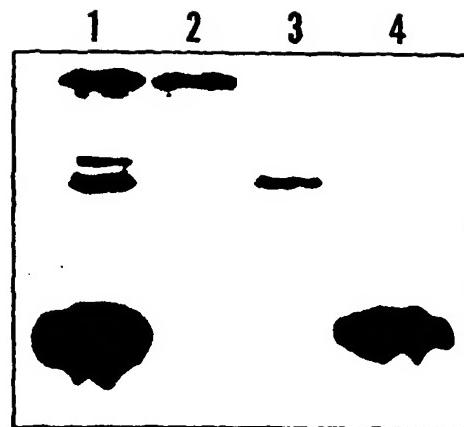
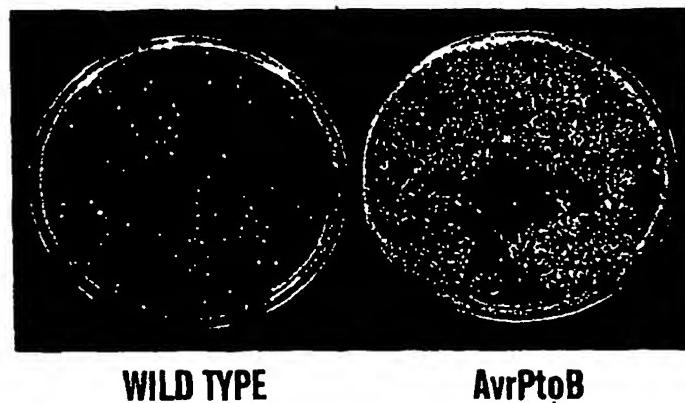
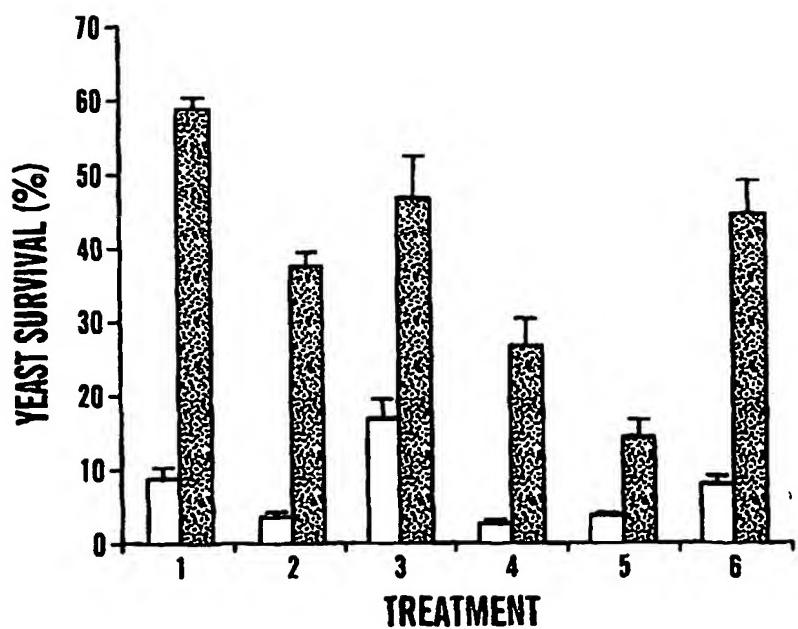


FIG. 1C

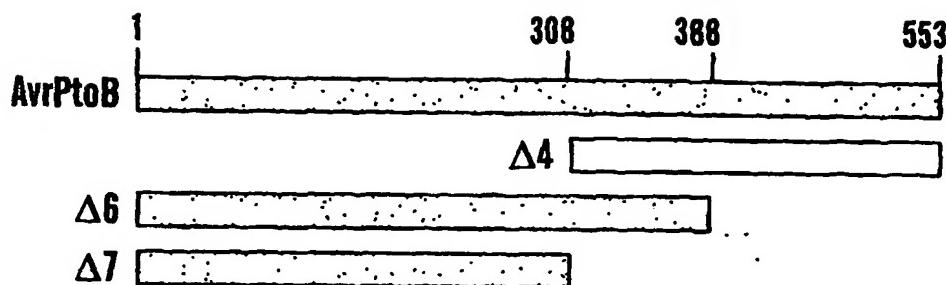
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**FIG. 2A****FIG. 2B**

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**FIG. 3A**

	RG-PtoR (<i>Pto/Pto</i> , <i>Prf/Prf</i>)	RG-Prf3 (<i>Pto/Pto</i> , <i>Prf3/Prf3</i>)	RG-Pto11 (<i>pto11/pto11</i> , <i>Prf/Prf</i>)	RG-ptoS (<i>pto/pto</i> , <i>Prf/Prf</i>)
AvrPtoB	+	-	-	-
Δ4	-	-	-	-
Δ6	+	-	+	-*
Δ7	+	-	-	-

FIG. 3B

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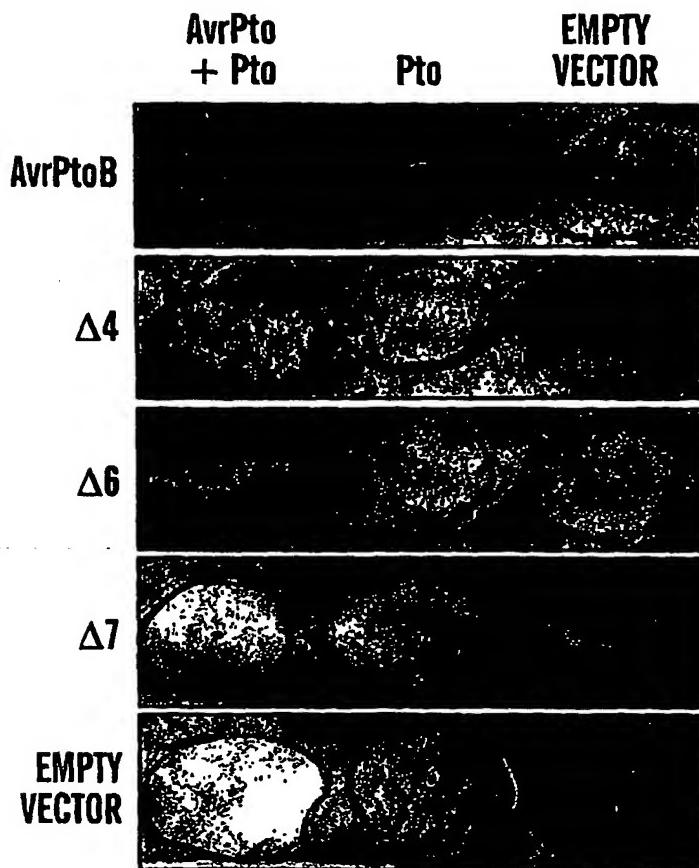


FIG. 4A

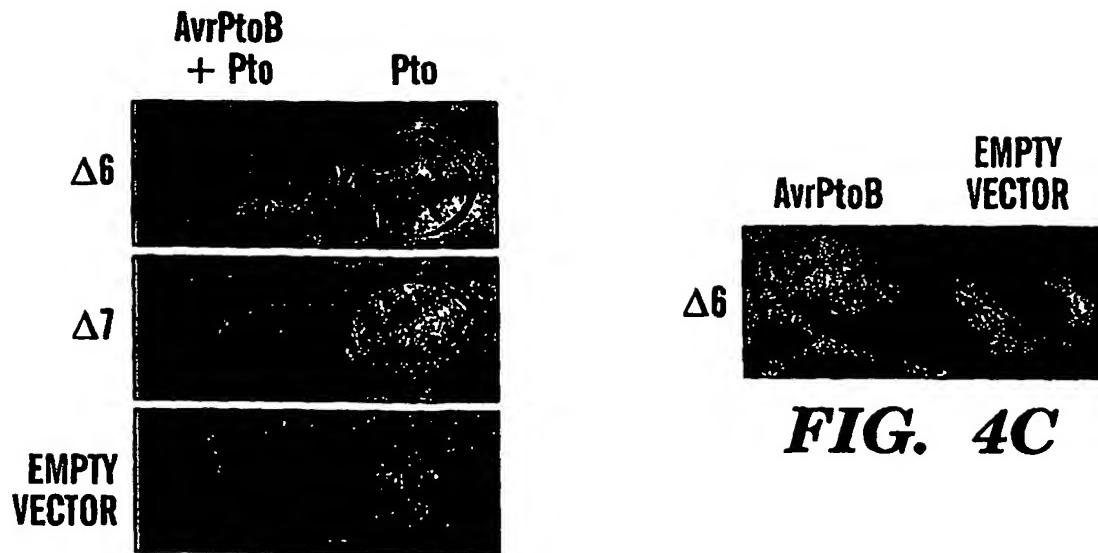
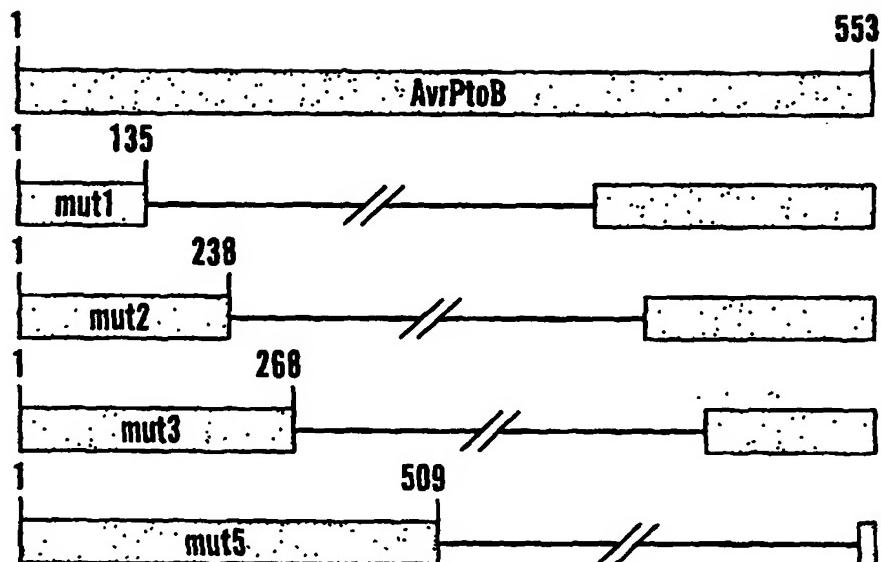


FIG. 4C

FIG. 4B

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**FIG. 5A**

	RG-PtoR (<i>Pto/Pto</i> , <i>Prf/Prf</i>)	RG-prf3 (<i>Pto/Pto</i> , <i>prf3/prf3</i>)	RG-ptol1 (<i>pto11/pto11</i> , <i>Prf/Prf</i>)	RG-ptoS (<i>pto/pto</i> , <i>Prf/Prf</i>)
AvrPtoB	I	D	D	D
mut1	I	D	D	D
mut2	I	D	D	D
mut3	I	D	D	D
mut5	I	D	I	D

FIG. 5B

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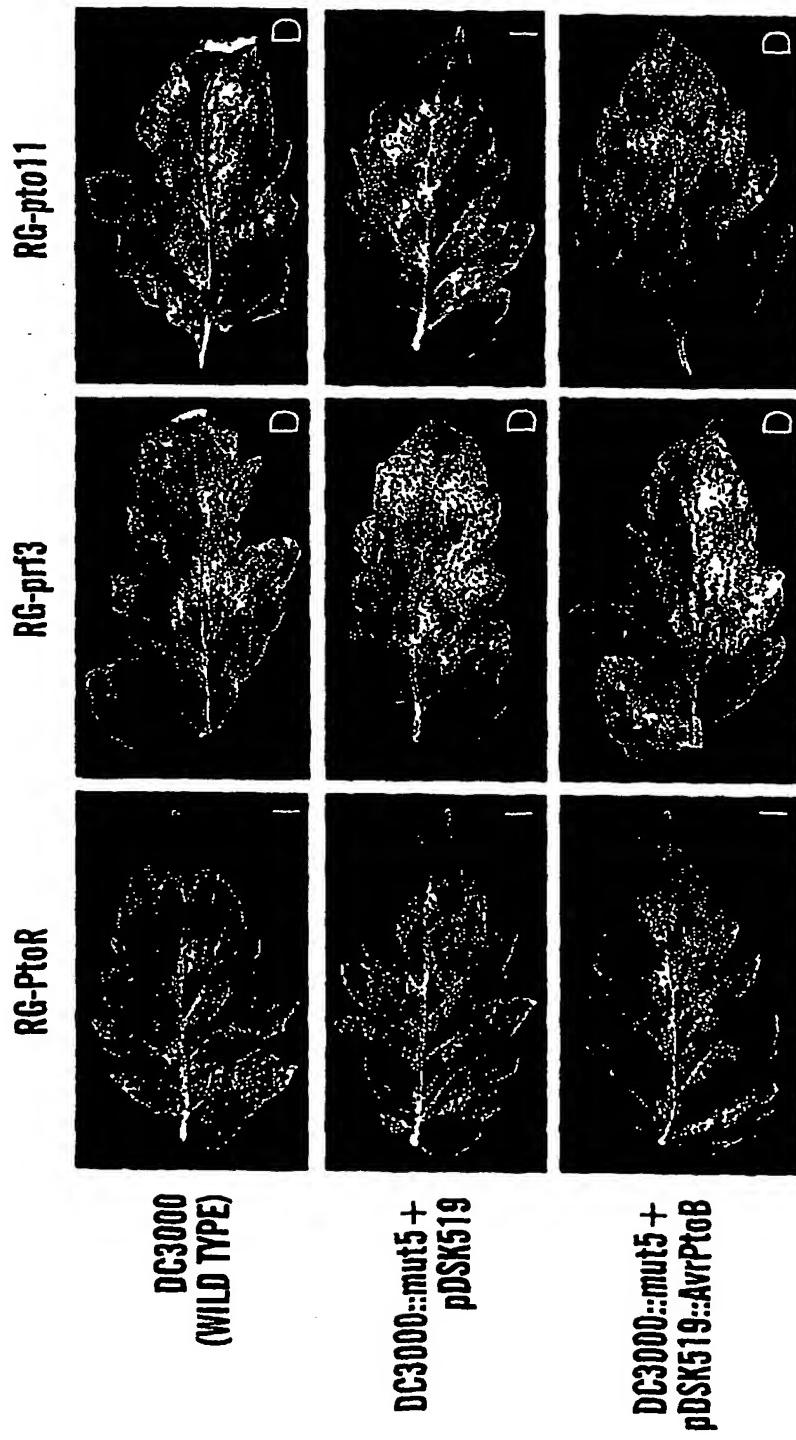


FIG. 6A

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- DC3000
- DC3000::mut5 + pDSK519
- ▼ DC3000::mut5 + pDSK519::avrPtoB

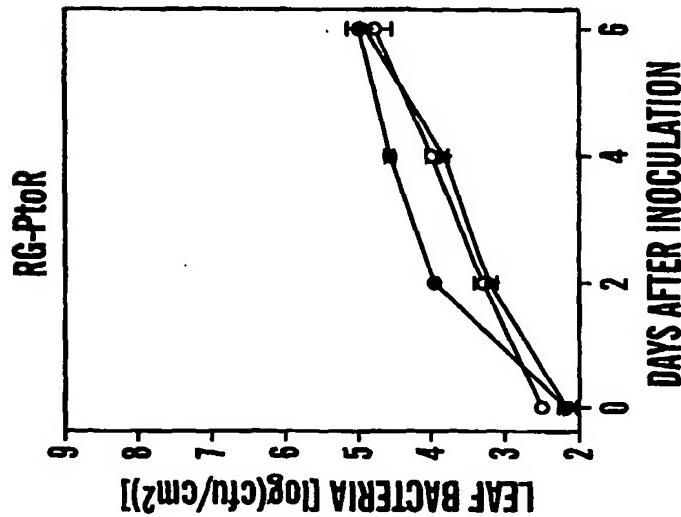
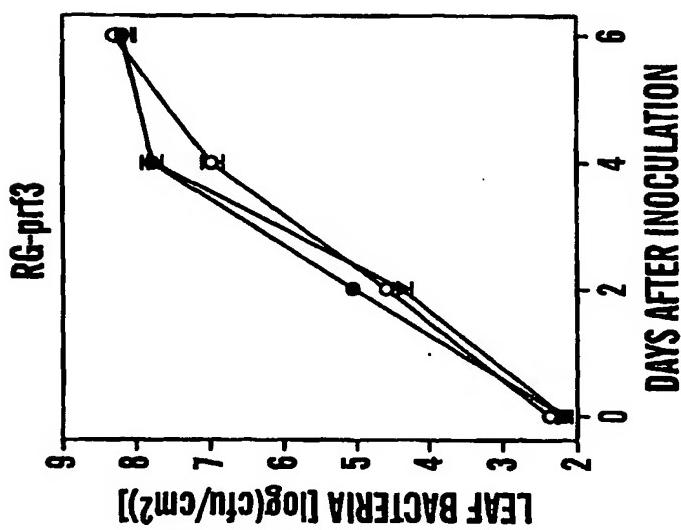
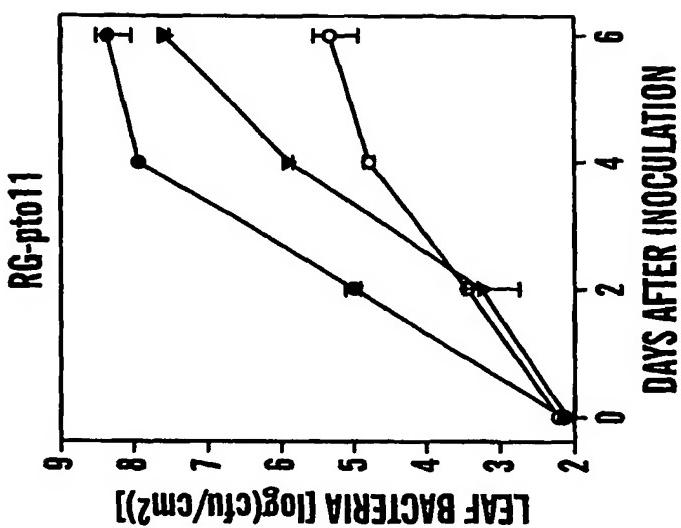


FIG. 6B

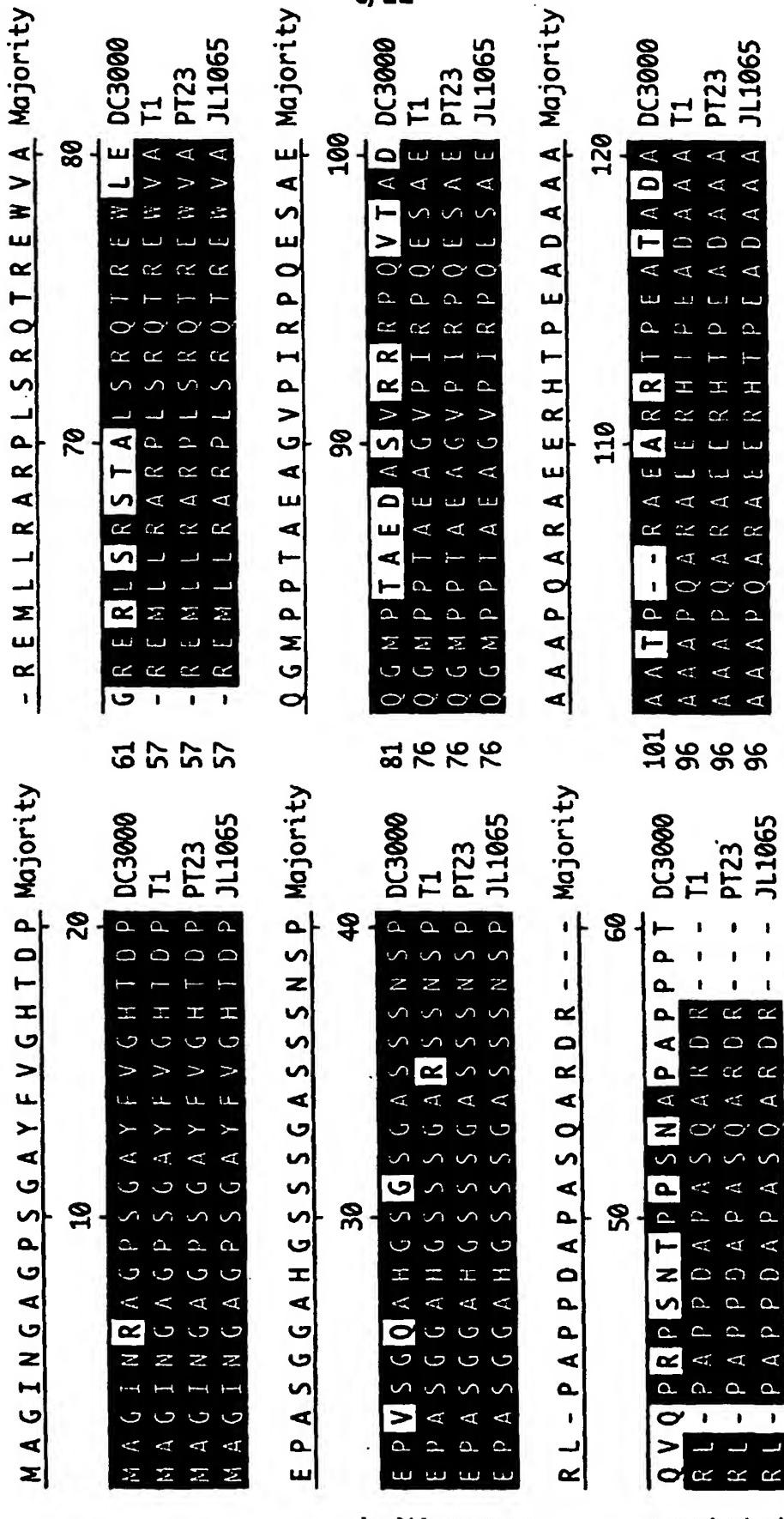


FIG. 7A

100 150 200

<u>S H V R T E G G R T P Q A L A G T S P R</u> Majority		<u>P S R T V Q S I L L I E H F P H L L A G E</u> Majority		<u>H F P N M P M H G</u> DC3000	
119	S - - - - -	- - - - A P R	DC3000	162	- S R V E Q N I F R Q
116	S H V R T E G G R T P Q A L A G T S P R	T1		176	P S R T V Q S I L L I E H F P H L L A G E
116	S H V R T E G G R T P Q A L A G T S P R	PT23		176	P S R T V Q S I L L I E H F P H L L A G E
116	S H V R T E G G R T P Q A L A G T S P R	JL1065		176	P S R T V Q S I L L I E H F P H L L A G E
<u>H T G A V P H A N R I V Q Q L V D A G A</u> Majority		<u>L I S G S E L A T A F R A A L R R E V R</u> Majority		<u>M a j o r i t y</u>	
123	R - G A V A H A N S I V Q Q L V S E G A	DC3000	181	I S R D S E L A T I E L	G A L R R A V H
136	H T G A V P H A N R I V Q Q L V D A G A	T1	196	L I S G S E L A T A F R A A L R R E V R	DC3000
136	H T G A V P H A N R I V Q Q L V D A G A	PT23	196	L I S G S E L A T A F R A A L R R E V R	T1
136	H T G A V P H A N R I V Q Q L V D A G A	JL1065	196	L I S G S E L A T A F R A A L R R E V R	PT23
<u>D L A G I N T M I D N A M R R H A I A L</u> Majority		<u>Q Q E A S A P P R T A A R S S V R T P E</u> Majority		<u>M a j o r i t y</u>	
142	D I S H T R N M L R N A M N G D A V A F	DC3000	201	Q Q A A S A P V R S P T P T	- - - - -
156	D L A C I N T M I D N A M R R H A I A L	T1	216	Q Q E A S A P P R T A A R S S V R T P E	DC3000
156	D L A C I N T M I D N A M R R H A I A L	PT23	216	Q Q E A S A P P R T A A R S S V R T P E	T1
156	D L A C I N T M I D N A M R R H A I A L	JL1065	216	Q Q E A S A P P R T A A R S S V R T P E	PT23

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<u>R S T V P P T S T E S S S G S N Q R T L</u>		<u>Majority</u>		<u>- G A N R V V M R N H G N N E A D A - - Majority</u>	
215	- - - - P A S P A A S S S G S S Q R S L	DC30000	268	- R V D R A A A M R N R G N D E A D A - - DC30000	310
236	R S T V P P T S T E S S S G S N Q R T L	T1	296	- G A N R V V M R N H G N N E A D A - - T1	320
236	R S T V P P T S T E S S S G S N Q R T L	PT23	296	- G A N R V V M R N H G N N E A D A - - PT23	
236	R S T V P P T S T E S S S G S N Q R T L	JL1065	296	- G A N R V V M R N H G N N E A D A - - JL1065	
<u>L G R F A G L M T P N Q R P S S A S N</u>		<u>Majority</u>		<u>A L O G L A O O G V D M E D L R A A L E Majority</u>	
270	F G R F A R L S A P N Q G R S S - - - N	DC30000	285	A l R G L V Q Q G V N L E H L R T I A L E DC30000	340
256	L G R F A G L M T P N Q R P S S A S N	T1	313	A l Q G L A Q Q G V D M E D L R A A L E T1	
256	L G R F A G L M T P N Q R P S S A S N	PT23	313	A l Q G L A Q Q G V D M E D L R A A L E PT23	
256	L G R F A G L M T P N Q R P S S A S N	JL1065	313	A l Q G L A Q Q G V D M E D L R A A L E JL1065	
<u>A S A S Q R P V D R S P P R V N Q V P T</u>		<u>Majority</u>		<u>R H I I L H R R P I P M D I A Y A L Q V Majority</u>	
290	T A A S Q T P V D R S P P R V N Q R P I	DC30000	305	R H V M Q R L P I P L D I I G S A L Q N V DC30000	360
248	A S A S Q R P V D R S P P R V N Q V P I	T1	333	R H I I L H R R P I P M D I A Y A L Q G V T1	
276	A S A S Q R P V D R S P P R V N Q V P I	PT23	333	R H I I L H R R P I P M D I A Y A L Q G V PT23	
276	A S A S Q R P V D R S P P R V N Q V P I	JL1065	333	R H I I L H R R P I P M D I A Y A L Q G V JL1065	

FIG. 7C

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<u>G I A P S I D T G E S L M E N P L M N L</u> Majority			
370	380	390	400
325 G I N P S I D L G E S L V Q H P L L N L DC30000	385 L R V M P E R E D Y E L N N V A Y G V R L	430	440
353 G I A P S I D T G E S L M E N P L M N L T1	413 L Q V I P A R E D Y E L N N V A Y G V R L		
353 G I A P S I D T G E S L M E N P L M N L PT23	413 L Q V I P A R E D Y E L N N V A Y G V R L		
353 G I A P S I D T G E S L M E N P L M N L JL1065	413 L Q V I P A R E D Y E L N N V A Y G V R L		

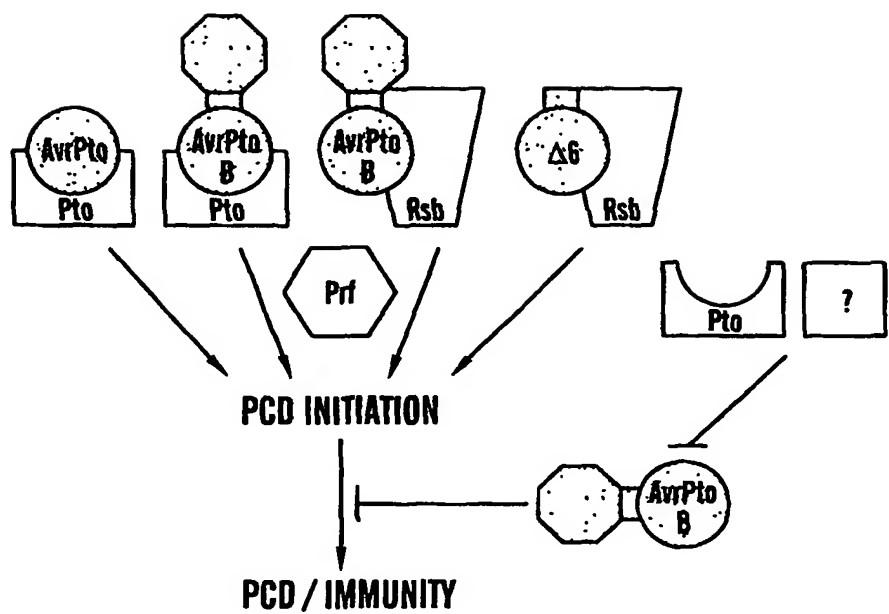
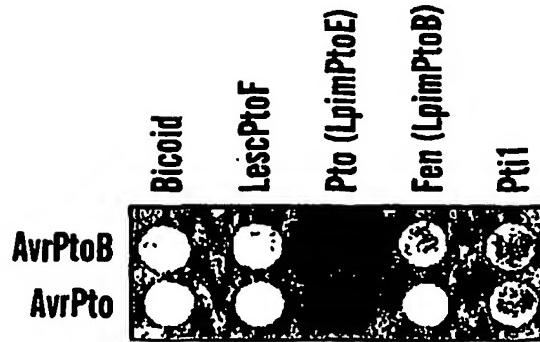
<u>S V A L H R A L G P R P A R A Q A P R P</u> Majority			
370	380	390	400
345 N V A L N R M L C L R P S A E R A P R P DC30000	405 L N L N P G V G V R Q A V A A F V T D R	450	460
373 S V A L H R A L G P R P A R A Q A P R P T1	433 L S L N P G A G V R E T V A A F V N N R		
373 S V A L H R A L G P R P A R A Q A P R P PT23	433 L S L N P G A G V R E T V A A F V N N R		
373 S V A L H R A L G P R P A R A Q A P R P JL1065	433 L S L N P G A G V R E T V A A F V N N R		
<u>A V P V A P A T V S R R P D S A R A T R</u> Majority			
410	420	430	440
365 A V P V A P A T A S R R P D G T R A T R DC30000	425 A E R P A V V A N I R A A L D P T I A S Q DC30000	470	480
393 A V P V A P A T V S R R P D S A R A T R T1	453 Y E R Q A V V A D I R A A L N - L S K Q T1		
393 A V P V A P A T V S R R P D S A R A T R PT23	453 Y E R Q A V V A D I R A A L N - L S K Q PT23		
393 A V P V A P A T V S R R P D S A R A T R JL1065	453 Y E R Q A V V A D I R A A L N - L S K Q JL1065		

FIG. 7D

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<u>F N K L R T V S K A D A A S N K P G F K</u> Majority				<u>S Y S R E A N K D L V F M D M K K L A Q</u> Majority
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***FIG. 8******FIG. 9A***

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Putative Hrp-box

```

1      ACAGTCCCCAGGGTGAATAGGAAAGGTGTGAT ggaaact CTTTCGTGCTCTTTGccac
61     ACAGCGCTGATCTTGCAGGTGATT CGGTCCGCAGGCAGAAGATCGGAGAGGATCAGCAT
121    ATGGCGGGTATCAATAGAGCGGGACCATCGGGCGCTTATT TGTGGCCACACAGACCCC
1      M A G I N R A G P S G A Y F V G H T D P
181    GAGCCAGTATCGGGCAAGCACCGGATCCGGCAGCGGCCAGCTCCTCGAACAGTCCG
21      E P V S G Q A H G S G S G A S S S N S P
241    CAGGTCAGCCCGGACCTCGAACATACTCCCCCGTCAAAGCGCCGGCACCGCCGAAACC
41      Q V Q P R P S N T P P S N A P A P P P T
301    GGACGTGAGAGGGCTTCA CGATCCACGGCCTGTCCGCGCAAACCAGGGAGTGGCTGGAG
61      G R E R L S R S T A L S R Q T R E W L E
361    CAGGGTATGCCAACAGCGGAGGTGCCAGCGTGCCTAGGCCACAGGTGACTGCCGAT
81      Q G M P T A E D A S V R R P Q V T A D
421    GCCGCAACGCCCGTGCAGAGGCAAGACGCCAGCGGGAGGCAACTGCCGATGCCAGCGCA
101    A A T P R A E A R R T P E A T A D A S A
481    CCGCGTAGAGGGCGGTGCAACGCCAACAGTATCGTCAGCAATTGGTCAGTGAGGGC
121    P R R G A V A H A N S I V Q Q L V S E G
541    GCTGATATTCGCATACTCGTAACATCGCTCCGAATGAAATGGCGACGCCAGTCGCT
141    A D I S H T R N M L R N A M N G D A V A
601    TTTTCTCGAGTAGAACAGAACATATTCGCCAGCATTCCCGAACATGCCCATGCAATGGA
161    F S R V E Q N I F R Q H F P N M P M H G
661    ATCAGCCGAGATT CGGA ACTCGCTATCGAGCTCCGTGGGCGCTCGTCGAGCGGTTCAC
181    I S R D S E L A I E L R G A L R R A V H
721    CAACAGGCGGCGTCAGGCCAGT GAGGTGCCAACCGGCCAGGCCCTGC GGCA
201    Q Q A A S A P V R S P T P T P A S P A A
781    TCATCATCGGGCAGCAGTCAGCGTTCTTTATTGGACGGTTGCCGTTGATGGCGCCA
221    S S G S S Q R S L F G R F A R L M A P
841    AACCAAGGGACGGTGTGCAACACTGCCCTCTCACAGCCGGTCGACAGGAGCCGCCA
241    N Q G R S S N T A A S Q T P V D R S P P
901    CGCGTCACCAAAAGACCCATACCGCTCGACAGGGCTCGATCGTAATCGTGGCAATGAC
261    R V N Q R P I R V D R A A M R N R G N D
961    GAGGCGGACGCCGGCTGGGGGGTAGTACAACAGGGGGTCAATTAGAGCCCTGCAC
281    E A D A A L R G L V Q Q G V N L E H L R
1021   ACGGCCCTGAAAGACATGTAATGCAGCGCTCCCTATCCCCCTCGATATAGGCAGCGCG
301    T A L E R H V M Q R L P I P L D I G S A
1081   TTGCAGAAATGTGGAAATTAAACCCAAAGTATCGACTGGGGAAAGCCTTGTGCAACATCCC
321    L Q N V G I N P S I D L G E S L V Q H P
1141   CTGCTGAATTGAAATGTAGCGTTGAATCGCATGCTGGGCTCGCTCCAGCGCTGAAAGA
341    L L N L N V A L N R M L G L R P S A E R
1201   GCGCCTCGTCCAGCCGTCCCCGGCTCCCGCAGCCCTCCAGGCAGCGATGGTACG
361    A P R P A V P V A P A T A S R R P D G T
1261   CGTGCACACGATTGCGGGTAGCCGGAGCGGGAGGATTACGAAAATAATGTGGCTTAT
381    R A T R L R V M P E R E D Y E N N V A Y
1321   GGAGTGCCTGCTTAACCTGAACCCGGGGTAGGCAGGCTGGCCCTT
401    G V R L L N L N P G V G V R Q A V A A F
1381   GTAACCGACCGGGCTGAGCGGCCAGCAGTGGTGGCTAATATCGGGCAGCCCTGGACCCCT
421    V T D R A E R P A V V A N I R A A L D P
1441   ATCGCGTCACAAATTCA GTGCGCACAATT CGAAGGCCATGCTGAATCTGAAGAG
441    I A S Q F S Q L R T I S K A D A E S E E
1501   CTGGGTTTAAGGATGCGGCAGATCATCACACGGATGACGTGACGCACTGTCTTTGGC
461    L G F K D A A D H H T D D V T H C L F G
1561   GGAGAATTGTCGCTGAGTAATCCGGATCAGCAGGTGATCGGTTGGGGGTAATCCGACG
481    G E L S L S N P D Q Q V I G L A G N P T
1621   GACACGTGCGAGCCTAACAGCCAAGAGGGAAATAAGGGACCTGGCGTTCATGGATATGAAA
501    D T S Q P Y S Q E G N K D L A F M D M K
1681   AAACCTGCCAACATT CCTCGCAGGAAGCCTGAGCATT CGATGCCGATGACCAAGAGAAACGCTAAC
521    K L A Q F L A G K P E H P M T R E T L N
1741   GCGAAAAATATGCCAACAGTATGCTTTAGAATAGTCCCtgaCCGCGCTGACAGCTAAAAA
541    A E N I A K Y A F R I V P
1801   GCCCATCAAGCTAGCGCCGACAGCGCTCACTGCCACTCGAAGGTGGCGTGGAAAGCTC
1861   CGGAGTCACGGACTTCGACCTCGCGTCAAGGGCTAGTCCATGCGCTCGGGTAGGTCA

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FIG. 9B

SUBSTITUTIONS -----

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- 52% identity of amino acid between AvrPtoB and VirPphA
- Black boxed letters: Putative hrp-box

- Red boxed letters: Computer suggested N-myristoylation site

1.	3- 8	GINRAG
2.	25- 30	GQAHGS
3.	29- 34	GSGSGA
4.	31- 36	GSGASS
5.	33- 38	GASSSN
6.	82- 87	GMPTAE
7.	140-145	GADISH
8.	278-283	GNDEAD
9.	288-293	GVSTTG
10.	294-299	GQFRAL
11.	325-330	GINPSI
12.	353-358	GLRPSA
13.	379-384	GTRATR
14.	412-417	GVRQAV
15.	480-485	GGELSL

- Black bold letters: Amino acid identical with amino acid of VirPphA

- Blue arrow: Fusion point of truncated AvrPtoB with LexA of prey vector

1. 70 AA; *HinP11*
2. 112 AA; *MspI*
3. 121 AA; *AcI*

FIG. 9B (CONT.)

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ALIGNMENT OF THE AMINO ACID SEQUENCES OF AvrPtoB AND VirPphA

BlastX results

Sequences producing significant alignments:

			Score (bits)	E Value
gi 5702216 gb AAD47203.1	AF141883_1 (AF141883) VirPphA [Pse...]	500	e-140	
gi 5702219 gb AAD47206.1	AF141883_4 (AF141883) unknown [Pse...]	70	6e-11	
gi 7512219 pir	T18535 high molecular mass nuclear antigen ...	50	6e-05	
gi 15236788 ref NP_194968.1	(NC_003075) putative protein [...]	45	0.002	
gi 5420387 emb CAB46679.1	(AJ243459) proteophosphoglycan [...]	45	0.003	
gi 6322209 ref NP_012284.1	(NC_001141) Required for invasi...	44	0.005	
gi 14251109 ref NP_116471.1	(NC_002794) t120 [Tupaia harpe...	43	0.008	
gi 4507349 ref NP_003176.1	(NM_003185) TATA box binding pr...	42	0.013	
gi 17546705 ref NP_520107.1	(NC_003295) PROBABLE TRANSMER...	42	0.013	
gi 15805485 ref NP_294181.1	(NC_001263) hypothetical prote...	42	0.013	
gi 17487943 ref XP_036528.2	(XM_036528) serine/arginine re...	42	0.018	

>gi|5702216|gb|AAD47203.1|AF141883_1 (AF141883) VirPphA [Pseudomonas syringae pv. phaseolicola] Length = 539

Score = 500 bits (1287), Expect = e-140
 Identities = 303/581 (52%), Positives = 368/581 (63%), Gaps = 28/581 (4%)
 Frame = +1

Query: 1	MAGINRAGPSGAYPVGHTDPEPVSGQAHGS...NSPQVQPRPNTTPSNAPAPPPT	180
Sbjct: 1	M GIN AGPS ++ TD EPV+ + H S ASS+NSP++ P S P +	51
	MPGINAGAPSNNFWQWRTDGEPVTEREHDS...SASSANSPELPPPAS-----PAES	
Query: 181	GRERLSRSTALS...RQTR...E...L...EQGMPTAEDASVRRR...PQVTADAATPRAEARRTPEATADASA	360
Sbjct: 52	GR+RL RS+ALSRQTR...E...A A V+ ATP AEAR++PEA	93
	GRQRLLRSE...ALSRQTR...E...-----ATPARVQ-----GATPPAEARQSPEAQ-----	
Query: 361	PRRGAVAHANSIVOQLVSEGADISHTR...MLRN...GDAVAFSRV...E...QNI FRQHFPN...PMHG	540
Sbjct: 94	A IVQ+LV GAD++ R MLRN M+ +AVAFSRV...E...I QHF...PMHG G	146
	-----QAERIVQELVRGGADLN...NVRTMLRN...M...NAVAFSRVERDILLQHF...PMHG	
Query: 541	ISRDSEL...L...E...LR...R...A...V...P...R...S...P...T...P...P...A...S...S...G...S...Q...S...L...F...G...R...F...A...R...L...M...A...P	720
Sbjct: 147	IS DS LA ELR LR+ V QQ R + TPA A SSSGSSQRSL GR LM P	200
	ISSDSVL...A...N...L...R...Q...L...R...Q...T...V...R...Q...-----RIQS...T...P...A...L...D...S...S...G...S...Q...S...L...I...G...R...S...T...M...L...M...T...P	
Query: 721	NQGRSSNTAA...S...Q...T...P...V...D...R...S...P...P...R...V...N...Q...R...P...I...R...V...D...R...A...M...R...N...R...G...N...D...E...A...D...A...A...L...R...G...L...V...Q...Q...G...V...N...L...E...H...L...R	900
Sbjct: 201	+ SS+ AAS+T VDR P ++ R+ AA N ++ + ALR L Q+GV++E LR	260
	GRS...SS...AA...A...S...R...T...S...V...D...R...P...Q...G...L...D...E...S...A...R...L...A...S...A...R...H...N...H...A...N...Q...T...M...E...A...L...R...L...T...Q...E...G...V...D...M...E...R...L...R	
Query: 901	TAI...L...R...H...V...N...Q...R...L...P...I...P...L...D...I...G...S...A...L...Q...N...G...I...N...P...S...I...D...L...G...E...S...L...V...Q...H...P...L...L...N...N...V...A...L...N...R...M...G...L...R...P...A...E...R	1080
Sbjct: 261	T+L R++M P+P D+ AL++VG...P I SLV HP+LN + ALN...R...L R +	320
	T...S...I...G...R...Y...I...M...S...L...E...P...L...P...D...L...R...R...A...L...E...S...V...G...I...N...P...F...I...P...E...E...L...S...L...V...D...H...P...V...I...N...F...S...A...L...N...R...M...L...A...R...Q...T...T...N	
Query: 1081	APRPAVPVAPATASRR-----PDGT---RAT...R...L...R...V...M...P...E...R...E	1176
Sbjct: 321	+P + A + RR P + RA RL VMP +	380
	S...P...E...L...P...P...L...A...S...E...G...R...R...L...L...R...S...P...P...L...L...S...G...Q...R...E...W...I...E...Q...S...M...R...Q...E...A...E...P...Q...S...S...R...L...N...R...A...V...R...L...A...M...P...P...Q...N	
Query: 1177	DYENNVAYGV...R...L...N...L...N...P...G...V...G...V...R...Q...A...A...F...V...T...D...R...A...E...P...A...V...V...A...N...I...R...A...A...L...D...P...I...A...S...Q...P...S...Q...L...R...T...I...S	1356
Sbjct: 381	+ E+NVAY +RL LNPG V + VA+F+TD A R VV +IRAALD IA QFSQLRTIS	439
	ENEDNVAYAIRL...R...R...L...N...P...G...A...D...V...S...V...V...A...S...P...I...T...D...P...A...A...R...Q...Q...V...V...N...D...I...R...A...A...L...D...-I...A...P...Q...F...S...Q...L...R...T...I...S	
Query: 1357	KADAEESELGP...K...D...A...D...H...H...T...D...D...V...T...H...C...L...F...G...G...E...L...S...L...S...N...P...D...Q...Q...V...I...G...L...A...G...N...P...T...D...T...S...Q...P...Y...S...Q...B...G...N...K	1536
Sbjct: 440	KADAEESELGP+D+AD H D+ T CLFG ELSLSNPDQOQVIGLA NPTD QFYSQE NK	498
	KADAEESELGP...R...D...A...D...-H...P...D...N...A...T...S...C...L...F...G...E...E...L...S...S...N...P...D...Q...Q...V...I...G...L...A...V...N...P...T...D...K...P...Q...Y...S...Q...E...V...N...K	
Query: 1537	DIAFM...D...N...I...K...L...A...Q...F...L...A...G...K...P...E...H...P...M...T...R...E...T...L...N...A...E...N...I...A...K...Y...A...P...I...V	1659
Sbjct: 499	L FMDM...D...K...L...A...Q...+...L...A...K...P...E...H...P...+...R...+...L...+...A...+...N...I...A...K...Y...A...P...+...I...V...P	539
	ALTPFM...D...N...I...K...L...A...Q...Y...L...A...D...K...P...E...H...P...L...N...R...Q...R...L...D...A...N...I...A...K...Y...A...P...I...V...P	

FIG. 9C

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	CHIMERIC	INTERACTION WITH: AvrPto	INTERACTION WITH: AvrPtoB
A	[solid black bar]	YES	YES
B	[white bar]	NO	NO
D	[white bar] [solid black bar]	NO	NO
E	[white bar] [white bar] [solid black bar]	NO	NO
F	[white bar] [white bar] [solid black bar] [white bar]	NO	NO
G	[solid black bar] [white bar] [solid black bar]	YES	YES
H	[solid black bar] [white bar] [white bar] [white bar]	NO	NO

FIG. 10A

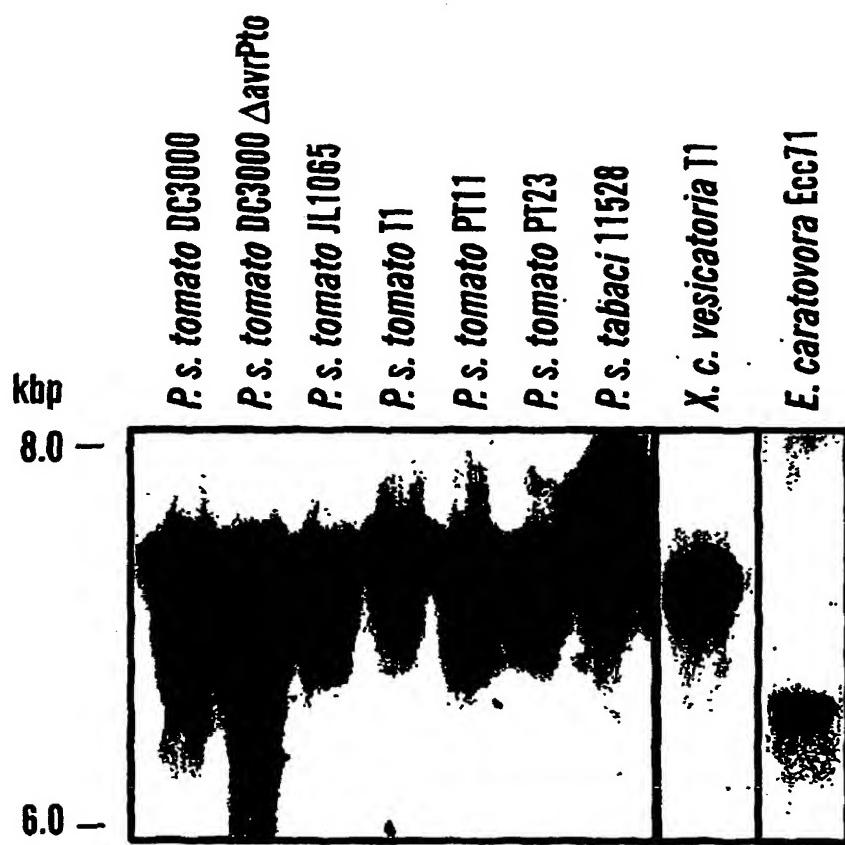
	INTERACTION WITH: AvrPto	INTERACTION WITH: AvrPtoB
FPB	YES	YES
FPB	133 217	
FPB2	YES	YES
FPB2	188 217	
FPB3	YES	YES
FPB3	202 217	
FPB4	YES	YES
FPB4	202 209	

FIG. 10B

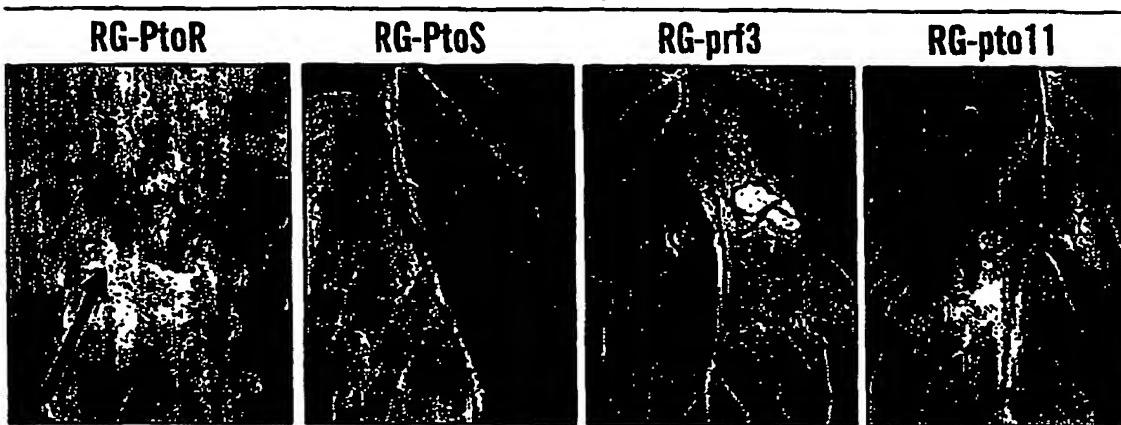
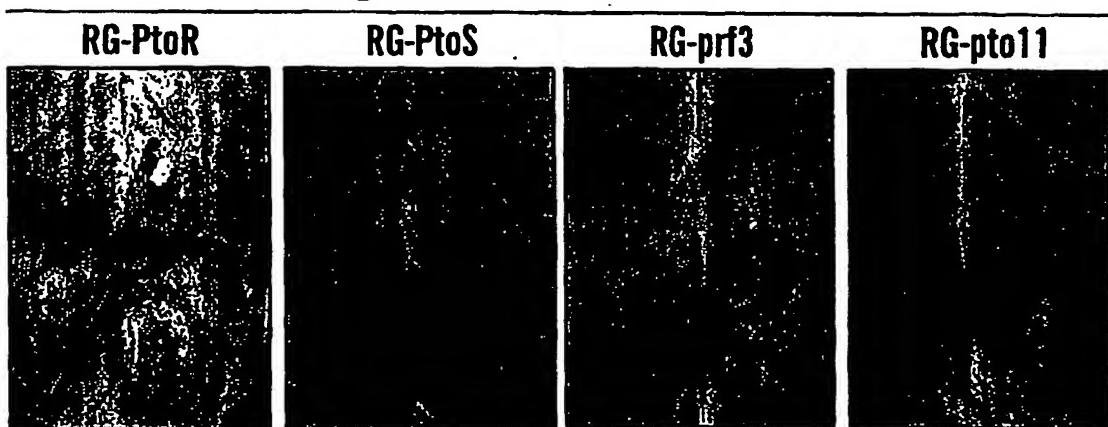
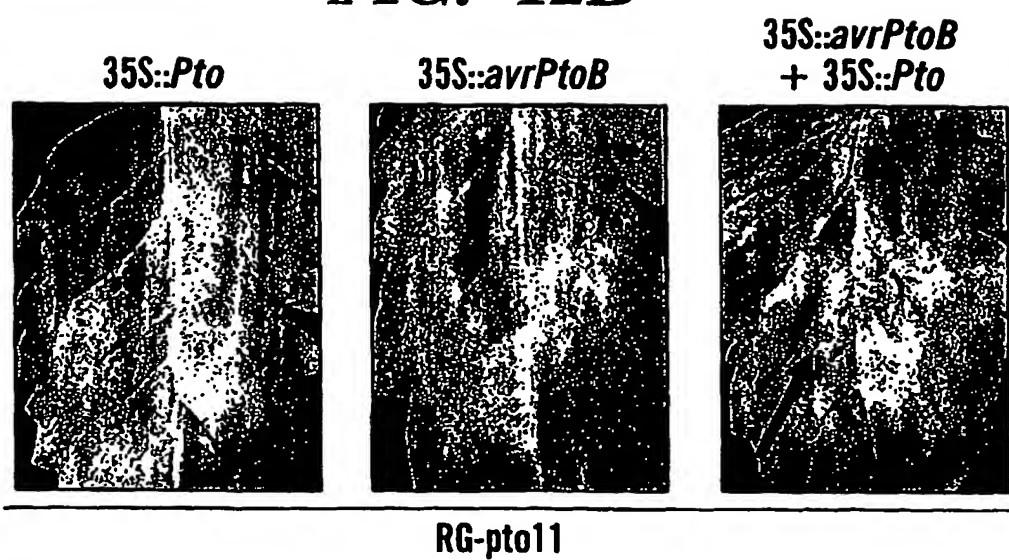
	102	204	205	209	INTERACTION WITH: AvrPto	INTERACTION WITH: AvrPtoB
Pto	[solid black bar]	K G T L G Y I D P E Y F I K G R			YES	YES
Fen	[white bar]	R G N I G Y I A P E Y A L W G Q			NO	NO
FPB3	[white bar]	K G T L G Y I D P E Y F I K G R			YES	YES
FPB4	[white bar]	K G P E G Y I D P E Y A L W G Q			YES	YES
FPB3(K202R)	[white bar]	R G P L G Y I D P E Y F I K G R			YES	YES
FPB3(T204N)	[white bar]	K G N L G Y I D P E Y F I K G R			NO	NO
FPB3(L205I)	[white bar]	K G T I G Y I D P E Y F I K G R			YES	YES
FPB3(D209A)	[white bar]	K G T L G Y I A P E Y F I K G R			YES	YES
P(T204N)	[solid black bar]	K G N L G Y I D P E Y F I K G R			NO	NO
P(L205I)	[solid black bar]	K G T I G Y I D P E Y F I K G R			YES	YES
F(N204T,1205L)	[white bar]	R G T L G Y I A P E Y A L W G Q			YES	YES
F(N204T)	[white bar]	R G T I G Y I A P E Y A L W G Q			YES	YES
F(1205L)	[white bar]	R G N L G Y I A P E Y A L W G Q			NO	NO

FIG 10C

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**FIG. 11**

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P. fluorescens (Hrp+, avrPtoB)**FIG. 12A***Agrobacterium (35S::avrPtoB)***FIG. 12B**

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Subregion

MAGINRAGPSGAYFVGHTDPEPVSGQAHSGSGASSNSPQVQPRPSNTP
MGNICVGG-----SRMAHQVNSPDRVSNNSGDE

I, II

PSNAPAPPPTGRERLSRSTALSRQTRWLEQGMPTAEDASVRRRPQVTAD
 DNVTSSQLLSVRHQLAESAGLPRDQHEFVSSQAP----QSLRNR-----
 AATPRAEARRTPEATADASAPRRGAVAHANSIVQQLVSEGADISHTRNML
 -----YNNL-----
 Δ121↓

III

RNAMNGDAVAFSRVEQNIFRQHPNMPMHGISRDSLAIELRGALRRAVH
 -----YSHTQRTLDADMQHRYMTGAS-----

IV

QQAAASAPVRSPTPTPASPAASSSGSSQRSLFGRFARLMAPNQGRSSNTAA

SQTPVDRSPPRVNQRPIRVDRAMRNNGNDEADAALRGLVQQGVNLHRL

ATA A A
 TALERHVMQRLLPIPLDIGSALQNV**GINP** SIDLGESLVQHPLLNLNALNR
 -----**GINP**-----GMLPHENVD-----

V

MLGLRPSAERA
 PRPAVPVAPATASRRPDGTRATRLRVM
 PEREDYENNVA
 DMR-SAITDW-----

VI

GVRLLNLNPVGVRQAVAAFVTDRAERPAVVANIRALA
 DPIASQFSQLRT
 SDMREAL-----

VII

ISKADAEEELGFKDAADHHTDDVTHCLFGGELSLSNP
 DQQVIGLAGNPT
 QHAMGIADIP

VIII

↑ CA40
 DTSQPYSQE
 GNKDLAFMDMKL
 LAQFLAGKPEHPMTRE
 TLNAE . . .
 PSUPERFVATMN-----
 PSGSIRMSTLSPS . . .

IX

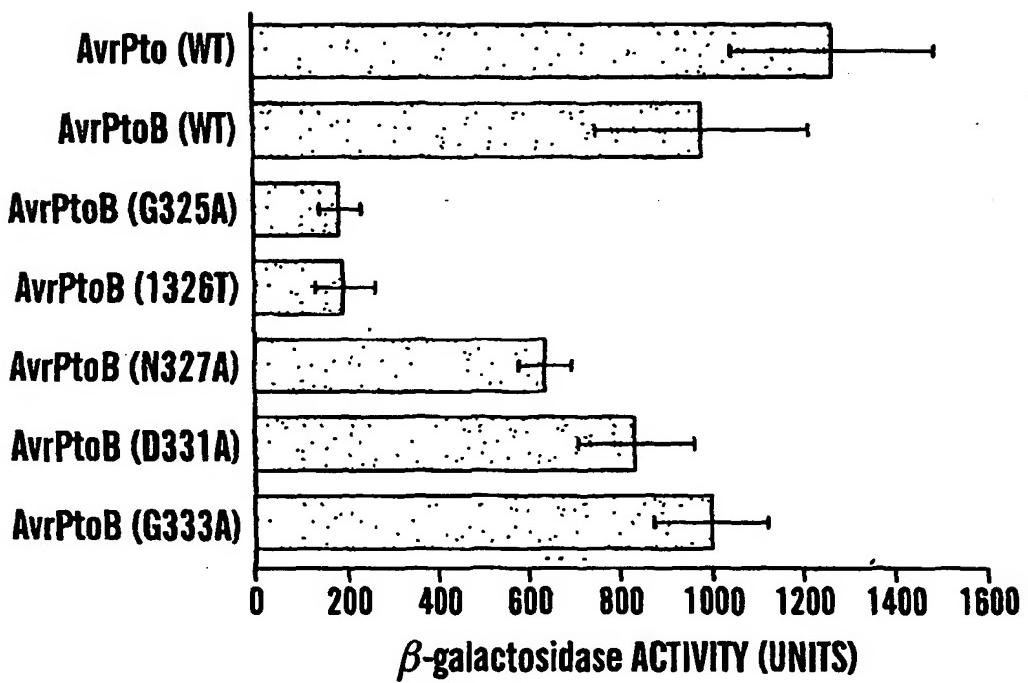
FIG. 13A

Consensus : SxRxxLxxSxxLxRxxxxE

AvrPto	38	SVRHQLAESAGLPRDQHE	55
AvrPtob	60	TGRERLSRSTALSRQTR	77
VirPphA	51	SGRQRLLRSSALSRQTR	68
AvrRpt2	49	ETRALLATKTVLGRHKIE	66
AvrRps4	38	TTTSIAQASEGLQRPGAT	55
AvrXa10	61	SPAFAFSAGSGFDLLRQFDP	78
AvrPpiB	41	IEEHVADRLSDLGRPDGG	58
AvrPphF	33	VGQYTLTSIHQLSSEERE	50
AvrBs1	49	RKRVIKENIAALHTSSLE	69
AvrB	33	SQRQLEVYDQCLIGAARW	50
AvrBsT	42	SPSQTSSAFSGLPERPRK	59

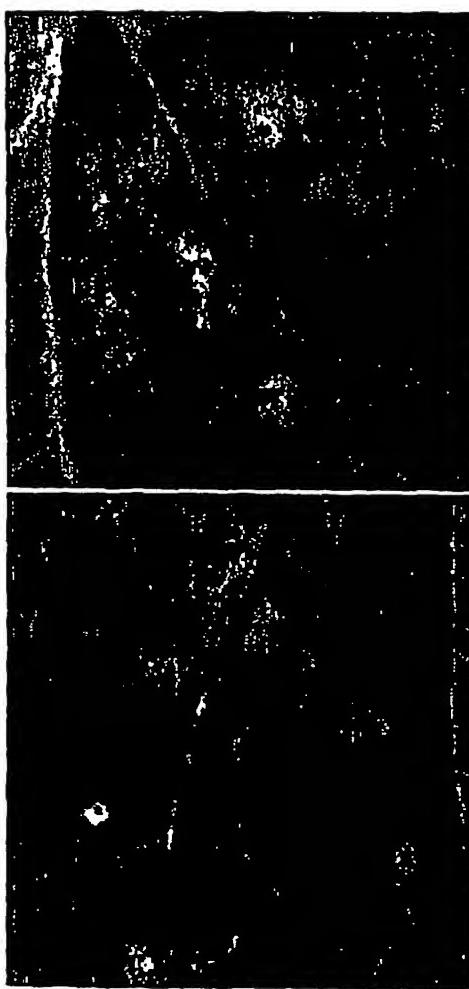
FIG. 13B

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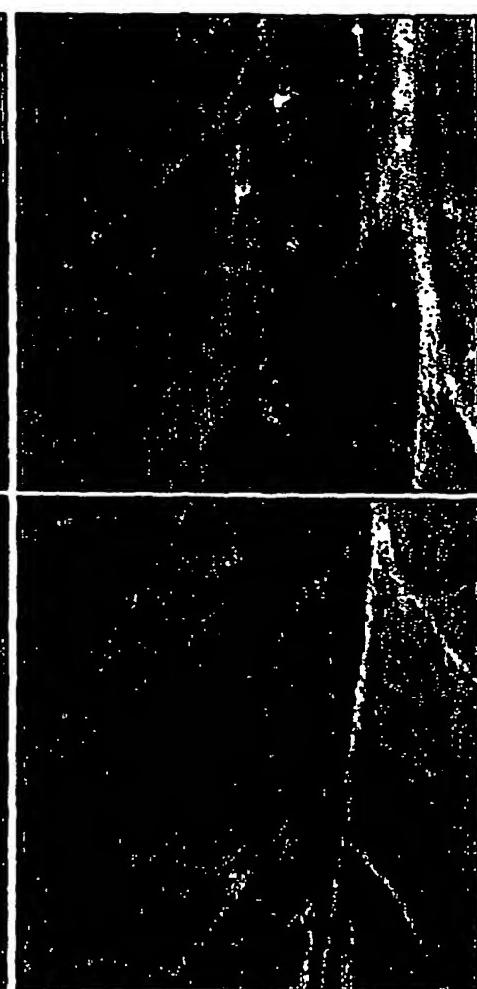
**FIG. 14**

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PT11



PT11 (AvrPtoB)



PT11
(AvrPtoB)

1326T MUTANT

PT11
(AvrPtoB)

G33A MUTANT

ALL LEAVES ARE Rio-Grande PtoR(*Pto/Pto*)

FIG. 15

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